

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/443,982ADATE: 04/17/96
TIME: 14:47:34

56

INPUT SET: S9946.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: DIXIT, VISHVA M.
6 O'ROURKE, KAREN
7
8 (ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING
9 FAS-ASSOCIATED APOPTOSIS
10
11 (iii) NUMBER OF SEQUENCES: 10
12
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: Morrison & Foerster
15 (B) STREET: 755 Page Mill Road
16 (C) CITY: Palo Alto
17 (D) STATE: CA
18 (E) COUNTRY: USA
19 (F) ZIP: 94304-1018
20
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Floppy disk
23 (B) COMPUTER: IBM PC compatible
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
26
27 (vi) CURRENT APPLICATION DATA:
28 (A) APPLICATION NUMBER: US 08/443,982
29 (B) FILING DATE: 18-MAY-1995
30 (C) CLASSIFICATION:
31
32 (viii) ATTORNEY/AGENT INFORMATION:
33 (A) NAME: Konski, Antoinette F.
34 (B) REGISTRATION NUMBER: 34,202
35 (C) REFERENCE/DOCKET NUMBER: 20344-21070.20
36
37 (ix) TELECOMMUNICATION INFORMATION:
38 (A) TELEPHONE: (415)813-5600
39 (B) TELEFAX: (415)494-0792
40 (C) TELEX: 706141 MRSNFOERS SFO
41
42
43 (2) INFORMATION FOR SEQ ID NO:1:
44
45 (i) SEQUENCE CHARACTERISTICS:
46 (A) LENGTH: 1642 base pairs

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47 (B) TYPE: nucleic acid
48 (C) STRANDEDNESS: single
49 (D) TOPOLOGY: linear
50
51 (ii) MOLECULE TYPE: cDNA
52
53
54 (ix) FEATURE:
55 (A) NAME/KEY: CDS
56 (B) LOCATION: 130..756
57
58 (ix) FEATURE:
59 (A) NAME/KEY: misc_feature
60 (B) LOCATION: 4..6
61 (D) OTHER INFORMATION: /note= "An in-frame stop codon 130
62 base pairs upstream of the initiator methionine"
63
64 (ix) FEATURE:
65 (A) NAME/KEY: polyA_signal
66 (B) LOCATION: 1636..1641
67 (D) OTHER INFORMATION: /note= "Potential poly(A)
68 adenylation signal"
69
70 (ix) FEATURE:
71 (A) NAME/KEY: misc_feature
72 (B) LOCATION: 198..753
73 (D) OTHER INFORMATION: /note= "Clone-15; 5' end of FADD"
74
75 (ix) FEATURE:
76 (A) NAME/KEY: misc_feature
77 (B) LOCATION: 249..753
78 (D) OTHER INFORMATION: /note= "Clone-8; 5' end of FADD"
79
80 (ix) FEATURE:
81 (A) NAME/KEY: misc_feature
82 (B) LOCATION: 177..658
83 (D) OTHER INFORMATION: /note= "Death Domain of FADD"
84
85 (ix) FEATURE:
86 (A) NAME/KEY: mutation
87 (B) LOCATION: replace(490..492, "aay")
88 (D) OTHER INFORMATION: /note= "For FADDmt: sequence is altered to either
89 the codon from Val to Asn"
90
91 (ix) FEATURE:
92 (A) NAME/KEY: misc_feature
93 (B) LOCATION: group(250..753, 232..753)
94 (D) OTHER INFORMATION: /note= "Codons can comprise
95 C-terminal polypeptide fragments of FADD"
96
97 (ix) FEATURE:
98 (A) NAME/KEY: misc_feature
99 (B) LOCATION: 253..753

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100      (D) OTHER INFORMATION: /note= "Codons can comprise
101 polypeptide fragment of FADD designated NFD-2"
102
103      (ix) FEATURE:
104          (A) NAME/KEY: misc_feature
105          (B) LOCATION: 310..753
106          (D) OTHER INFORMATION: /note= "Codons can comprise
107 polypeptide fragment of FADD designated NFD-3"
108
109      (ix) FEATURE:
110          (A) NAME/KEY: misc_feature
111          (B) LOCATION: 367..753
112          (D) OTHER INFORMATION: /note= "Codons can comprise
113 polypeptide fragment of FADD designated NFD-4"
114
115      (ix) FEATURE:
116          (A) NAME/KEY: misc_feature
117          (B) LOCATION: 131..504
118          (D) OTHER INFORMATION: /note= "Codons can comprise an
119 N-terminal half polypeptide fragment of FADD designated N-FADD"
120
121      (ix) FEATURE:
122          (A) NAME/KEY: misc_feature
123          (B) LOCATION: 133..501
124          (D) OTHER INFORMATION: /note= "Codons can comprise an
125 N-terminal half polypeptide fragment of FADD"
126
127
128      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
129
130      CTCTAAAGGT TCGGGGGTGG AATCCTTGGG CCGCTGGGCA AGCGGCGAGA CCTGGCCAGG      60
131
132      GCCAGCGAGC CGAGGACAGA GGGCGCACGG AGGGCCGGGC CGCAGCCCCG GCCGCTTGCA      120
133
134      GACCCCGCC ATG GAC CCG TTC CTG GTG CTG CTG CAC TCG GTG TCG TCC      168
135      Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser
136      1 5 10
137
138      AGC CTG TCG AGC AGC GAG CTG ACC GAG CTC AAG TTC CTA TGC CTC GGG      216
139      Ser Leu Ser Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly
140      15 20 25
141
142      CGC GTG GGC AAG CGC AAG CTG GAG CGC GTG CAG AGC GGC CTA GAC CTC      264
143      Arg Val Gly Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu
144      30 35 40 45
145
146      TTC TCC ATG CTG CTG GAG CAG AAC GAC CTG GAG CCC GGG CAC ACC GAG      312
147      Phe Ser Met Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu
148      50 55 60
149
150      CTC CTG CGC GAG CTG CTC GCC TCC CTG CGG CGC CAC GAC CTG CTG CGG      360
151      Leu Leu Arg Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg
152      65 70 75

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206 GGACACTAGG GTCAGGCGGG GTGCTGTGGT GGGGAGAGGC ATGGCTGGGG TGGGGGTGGG 1336
207
208 GAGACCTGGT TGGCCGTGGT CCAGCTCTTG GCCCCTGTGT GAGTTGAGTC TCCTCTCTGA 1396
209
210 GACTGCTAAG TAGGGGCAGT GATGGTTGCC AGGACGAATT GAGATAATAT CTGTGAGGTG 1456
211
212 CTGATGAGTG ATTGACACAC AGCACTCTCT AAATCTTCCT TGTGAGGATT ATGGGTCCTG 1516
213
214 CAATTCTACA GTTCTTACT GTTTTGTATC AAAATCACTA TCTTTCTGAT AACAGAATTG 1576
215
216 CCAAGGCAGC GGGATCTCGT ATCTTTAAAA AGCAGTCCTC TTATTCCTAA GGTAATCCTA 1636
217
218 TTAAAA 1642
219
220

221 (2) INFORMATION FOR SEQ ID NO:2:

222
223 (i) SEQUENCE CHARACTERISTICS:
224 (A) LENGTH: 208 amino acids
225 (B) TYPE: amino acid
226 (D) TOPOLOGY: linear
227

228 (ii) MOLECULE TYPE: protein
229

230 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

231
232 Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser Ser Leu Ser
233 1 5 10 15
234
235 Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly Arg Val Gly
236 20 25 30
237
238 Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu Phe Ser Met
239 35 40 45
240
241 Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg
242 50 55 60
243
244 Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg Arg Val Asp
245 65 70 75 80
246
247 Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly Glu Glu Asp
248 85 90 95
249
250 Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly Lys Asp Trp
251 100 105 110
252
253 Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys Ile Asp Ser
254 115 120 125
255
256 Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val Arg Glu Ser
257 130 135 140
258

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SEQUENCE VERIFICATION REPORT
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Line	Error	Original Text
271	Stop Codon at end of sequence removed - no error	